

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2003, 22:00:37 ; Search time 37 Seconds
(without alignments)
1884.108 Million cell updates/sec

Title: US-09-815-923-4
Perfect score: 3141
Sequence: 1 MPSPDAPPATPPDLPAT.....TIQREVTSTPPADSTLCNL 587

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues
Minimum number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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- 17: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3141	100.0	587	11	US-09-815-923-4
2	2333.5	74.3	622	10	US-09-843-598-11
3	1726	55.0	630	10	US-09-843-598-10
4	1579.5	50.3	671	10	US-09-843-598-5
5	1571.5	48.0	671	10	US-09-843-598-7
6	1532.5	48.8	624	10	US-09-795-693-24
7	1532.5	48.8	624	15	US-10-156-239-24
8	1532.5	48.8	624	15	US-10-156-239-24
9	1369.5	43.6	797	10	US-09-795-485-24
10	1302	41.5	597	11	US-09-815-923-2
11	1247.5	39.7	614	12	US-09-919-039-378
12	1221	38.9	727	11	US-09-815-923-10
13	1077	34.3	421	10	US-09-843-598-9
14	1069	34.0	556	11	US-09-815-923-6
15	990	31.5	437	11	US-09-818-656A-4
16	990	31.5	437	15	US-10-216-441-4

17	990	31.5	459	11	US-09-818-656A-2	Sequence 2, Appli
18	990	31.5	459	15	US-10-216-441-2	Sequence 2, Appli
19	981	31.2	730	10	US-09-741-149-2	Sequence 2, Appli
20	981	31.2	730	10	US-09-795-693-5	Sequence 5, Appli
21	981	31.2	730	15	US-10-156-239-5	Sequence 5, Appli
22	981	31.2	730	15	US-10-199-485-5	Sequence 5, Appli
23	973	31.0	729	10	US-09-741-149-4	Sequence 4, Appli
24	964.5	30.7	599	11	US-09-861-846-4	Sequence 4, Appli
25	960	30.6	676	11	US-09-815-923-12	Sequence 12, Appli
26	943.5	30.0	610	11	US-09-861-846-2	Sequence 2, Appli
27	926.5	29.5	727	10	US-09-923-444A-2	Sequence 2, Appli
28	618	19.7	579	11	US-09-738-626-4648	Sequence 4648, Ap
29	461.5	14.7	224	10	US-09-843-598-6	Sequence 6, Appli
30	300	9.6	449	12	US-09-769-787-110	Sequence 110, App
31	167	5.3	196	12	US-09-989-442-87	Sequence 87, Appli
32	142	4.5	52	10	US-09-864-761-43363	Sequence 43363, A
33	136	4.3	1098	11	US-09-712-363-288	Sequence 288, App
34	133.5	4.3	84	10	US-09-864-761-39755	Sequence 39755, A
35	118.5	3.8	77	10	US-09-864-761-39850	Sequence 39850, A
36	117	3.7	403	15	US-10-140-372-2	Sequence 2, Appli
37	116	3.7	489	15	US-10-156-761-8760	Sequence 8760, Ap
38	111.5	3.5	442	15	US-10-156-761-9153	Sequence 9153, Ap
39	111	3.5	475	10	US-09-815-242-11503	Sequence 11503, A
40	110	3.5	505	12	US-09-769-787-11388	Sequence 120, App
41	109.5	3.5	519	10	US-09-815-242-11388	Sequence 11388, A
42	109.5	3.5	519	11	US-09-895-913A-118	Sequence 118, App
43	109.5	3.5	1083	14	US-10-080-170-330	Sequence 330, App
44	109	3.5	553	12	US-09-836-705-38	Sequence 38, Appli
45	108	3.4	510	10	US-09-815-242-13607	Sequence 13607, A

ALIGNMENTS

RESULT 1
US-09-815-923-4
; Sequence 4, Application US/09815923
; Publication No. US20020197644A1
; GENERAL INFORMATION:
; APPLICANT: G111, Sarjeet S.
; APPLICANT: Ross, Linda S.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815, 923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: sectionin transporter
US-09-815-923-4

Query Match 100.0%: Score 3141; DB 11; Length 587;
Best Local Similarity 100.0%: Pred. No. 6.7e-274;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPDAPPATPPDLPATTAOKSRVSVSLTPARQRETMWAKAEFLLAVFADLGN 60
1 MPSPDAPPATPPDLPATTAOKSRVSVSLTPARQRETMWAKAEFLLAVFADLGN 60
Db 1 MPSPDAPPATPPDLPATTAOKSRVSVSLTPARQRETMWAKAEFLLAVFADLGN 60
QY 61 VMFPFICVONGGAFILPCVWMLFGGLDFLELALGQYHRCGLTLMKRCPALUKV 120
61 VMFPFICVONGGAFILPCVWMLFGGLDFLELALGQYHRCGLTLMKRCPALUKV 120
Db 61 VMFPFICVONGGAFILPCVWMLFGGLDFLELALGQYHRCGLTLMKRCPALUKV 120
QY 121 GYACIMDIYMGWYNTIIGWAVYVLIASIASINSVLPMTSCDNEWNTPLCTPVTSPQTN 180
121 GYACIMDIYMGWYNTIIGWAVYVLIASIASINSVLPMTSCDNEWNTPLCTPVTSPQTN 180
Db 121 GYACIMDIYMGWYNTIIGWAVYVLIASIASINSVLPMTSCDNEWNTPLCTPVTSPQTN 180

OY	181	NNSSRPAKEEPPERNVLEQHKSNGLDDMGIRKSLACVGVVLVYFSLMKGVRSAGKV	240
Db	181	NNSSRPAKEEPPERNVLEQHKSNGLDDMGIRKSLACVGVVLVYFSLMKGVRSAGKV	240
OY	241	WTALAPVVLILLILARGVTLTPGATEGIRYYLTPENHKIQNSKVMWIDAASQIFPSGPGF	300
Db	241	WTALAPVVLILLILARGVTLTPGATEGIRYYLTPENHKIQNSKVMWIDAASQIFPSGPGF	300
OY	301	GTLLASSYNNKFNNNCYRDALITSSINCLTSLFAGVIFSVLGMAHYONKSIEEYGLEG	360
Db	301	GTLLASSYNNKFNNNCYRDALITSSINCLTSLFAGVIFSVLGMAHYONKSIEEYGLEG	360
OY	361	PGIVFIYVPEALATMTGVSFWMAIIFFMLITIGLDBSTFEGGLEAVTALCDEYPRVLGRHR	420
Db	361	PGIVFIYVPEALATMTGVSFWMAIIFFMLITIGLDBSTFEGGLEAVTALCDEYPRVLGRHR	420
OY	421	EVFVAVLLLEFYICALPTTYYGCVLVLDLNNYGPCLALLFVFAEAGVCWYGVDRFS	480
Db	421	EVFVAVLLLEFYICALPTTYYGCVLVLDLNNYGPCLALLFVFAEAGVCWYGVDRFS	480
OY	481	EDVRTMLGHTPGCFWRTCMYSISPVELLVLFVFSVLAHEEMLGEEYTPSMTITVGWYMT	540
Db	481	EDVRTMLGHTPGCFWRTCMYSISPVELLVLFVFSVLAHEEMLGEEYTPSMTITVGWYMT	540
OY	541	GTYSVCIPLYITIKLLITPGNCINAKTIQREYVSIIPADSTLCML	587
Db	541	GTYSVCIPLYITIKLLITPGNCINAKTIQREYVSIIPADSTLCML	587

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Db      281 YVVLLILLVAGVSLPADSGIKYUULPRENNIKAKSNKWIDAQQIFLSRGGEGTLLALS 340
Qy      308 SYKNFNNNCYRDALITSSINCLTSFLAGFVFSVLGMAHVONKSIEEVLGECGLVFIV 367
        |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      341 SYKFNFNNCYRDALITSSINCLTSFLAGFVFISVLGMAYVQKSIDRVGLEGCGLVFIV 400
Qy      368 YPRFIATMGSYVMALLFFMLLTIGLDBSTBEGGLEAVYTALCDEYPRYLGRHREPVAVL 427
        |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      401 YPRFIATMSGSYVMSTIFFLMELTIGLDBSTBEGGLEAMTALCDEYPRYIGRRRLFYLL 460
Qy      428 LLEFYICALPTTYTGVSGLVLDLLLNLYGRCALILFVFAEAGVCWVGVDRESDDVTML 487
        |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      461 LAEIFCALPRTMYGVSGLVYNFLNLYGRCALILFVFAEAGGVEMFTGVDRESDDVQML 520
Qy      488 GHTPGWFMTQWSYISPFVELLVLFVFSYLAHEMLGGEYTPSKMSITGVGMVGTCTVSCI 547
        |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      521 GSRPGLEFMRIOWYISVPFLTLTFIIFSINGXYEMLGEEYYPDMSYGMAVTCSSVLGI 580
Qy      548 PLYITYKKLLI-TPGNCSINRIKITIQORE 573
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Db      581 PMYIIYKFEPFASKGCGCRORLOESFOPE 607

RESULT 3
US-09-843-598-10
; Sequence 10, Application US/09843598
; Patent No. US20020010944A1
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RESULT 2
US-09-843-598-11
Sequence 11, Application US/09843598
Patent No. US2002010944A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESTR GENES, PROTEINS, AND MODULATORY
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 01997/525002
CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 622
TYPE: PRT
ORGANISM: Drosophila melanogaster
09-843-598-11

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        6  APPAPTAAPP---DLDPATTAACKSRVVVSLTPARORETMAKKAPELLVWGFAVDLGNW 62
        55.0%:  Score 1726;  DB 10;  Length 630;
        54.5%:  Pred. No. 1,3e-146;
        97;  Mismatches 154;  Indels 16;  Gaps 6

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	Query Match	74.3%	Score 233.5	DB 10	Length 622
	Best Local Similarity	76.5%	Pred. No. 3e-201		
	Matches	Conservative	50	Mismatches	76; Indels 7; Gaps 4
Qy	8	PAPAPPPDLPATTAQAQSRKSVVSLTPAQRQRETMWAKAEFLAVGVFAVDLGNVRFPYI	67		
Dd	47	PAKYTD--LAPKLANNERILVYST-EETRETWGACAFELLAIVGFAVDLGNVRFPYI	103		
Qy	68	CYONGGAFLIPCYMLFGGLPFFLELALGYHRGCGLTLMKRICPALKGVAIGMI	127		
Dd	104	CYONGGAFLVPYCFLIFGGLPYEMETALQFHRCCGLSTIMKRICPALKGVAICLI	163		
Qy	128	DIYMGMYNTIIIGAAVVYLIASINSVLPTSCDNEMNPTPLCTPTYSPOTPNASTPA	187		
Dd	164	DIYMKYNTIIIGAAVVYL--FAEFTSKLPTSCDNPNENTENCMOVTSENFTELATSPA	220		
Qy	188	KEFEERNVLEOHKSNGLDMPGIRKESLACVGVEVLVFSLMKGVSAGKVVMYTALAP	247		
Dd	221	KEFEERKKLVESKGGDLPMGPVKRTTLACVGEVVLVFSLMKGVSAGKVVMYTALAP	280		
Qy	248	VYVLLILLARGVLTGATEGRIVYLLPEWHKLQNSKWIDAASQIEFSLSGPGFTLLAS	307		

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Db      49  AVSPGAGDDTRISIPATT-----TTVAELHQGREHWGKKVDFLLSYGVANDLGNW 103
QY      63  RPPYICYONGGAGFELLPYCVMLFSGBLPFELETALGOYHRCGLTLMKRICPALKGVY 122
      104  RPPYICYONGGAGFLLPYTIMAFEGIPLPFVELLALGQYHRCGCSITMRKICPFKIGY 163
Db      123  ALCIMIDYMGMYNTTICGAVYYLLASLASINSVLPMTSCNENANTPLCIPVSPQ--- 179
QY      164  ALCILFAYLASYYNTTMAVALYYLL---SSFTDQLPMTSCNSWNTGNCYNESEDNTIW 220
Db      180  NPNSSIPAKEFEFRNRYLEQHSNGSDDDMGPIKPSLALCFVPLAVFYELFMKGVRSGKV 239
QY      221  TLHSTSPAEFFRYTHRYLQIHRSKGIQDDLGISWQALCALCMLPFYIVYFSTMRKGVKTSKV 280
Db      240  VMTALAPYVLLILLARGVTLPGATEGIRYVLLPEMHKLONSKYVMDAASQIIFSLGPG 299
QY      281  VMTATPEFYITLSVLLRGATPLPGAMRGVLFYLPKPNMKLLETGTWMDAAAQIFFSLGPG 340
Db      300  EGYLLALSSYNNKFNNGCYDALITSSINCLNSFLAGVYTESVGLQYMAHYONKSIEVEYGL 359
QY      341  EGYLLAFASYNKFNNGCYDALVYTSVVMQMTSPFVSGVIFIVLGLGYMAEMRNEDEVAYKD 400

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QY 360 -GPGLVFVYPPALATMGSGVMAIFLMLTLTGLDSTFGGLEAVTTALCDEYPRVLGR 418
DB 401 AGPSLFLTYAFAIANMPASTFEALIFLMLTLTGLDSTFGGLEAVTTALCDEYPRVLGR 460
QY 419 HREYVAVALLFTYICALFTTYGGVYLVDLNVPGLAIFVYFAEAGACWYGVDR 478
DB 461 RREYVAVALLFTYICALFTTYGGVYLVDLNVPGLAIFVYFAEAGACWYGVDR 520
QY 479 FSEDYRTMLGTHPGWFMTGWSYISPVFLVLFVSVLAHEMLGEYTPSPMSITVGMV 538
DB 521 FCRDVKEMHGFSPGFWFRICWVAISPLFLITICSLMSPPOURLFQYVYPMWISITLGYC 580
QY 539 MTGTVSCIPLYIYKLLTPGNCINR-1KTQREYVTSIPPADSTL 584
DB 581 ICTSSFCIPYIAYRLITPGTFKRIKSTIPPEPTEIPGDIRL 627

RESULT 4
US-09-843-598-5
Sequence 5, Application US/09843598
Patent No. US20020010944A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESERT GENES, PROTEINS, AND MODULATORY
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 01997/525002
CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 671
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-843-598-5

Query Match 50.3%; Score 1579.5; DB 10; Length 671;
Best Local Similarity 48.7%; Pred. No. 2.1e-133;
Matches 300; Conservative 110; Mismatches 161; Indels 45; Gaps 11;

QY 9 APTAPPDLPATTAAKRSRSVVS-----LTPARQ-----RE 39
DB 43 APTA-SEVWPLSVADKPLTLVSTSHSIDPNEPIALGSLTPKBEYVALRRSSMVAD 101
QY 40 TWAKKAEPFLAVVGAFAVDLGNWREPYICYONGGAFLLPYCYMLLFGGLPFFLELALG 99
DB 102 KWATKMEFLAVVGAFAVDLGNWREPYICYONGGAFLLPYCYMLLFGGLPFFLELALG 161
QY 100 QYHRCGLTLMKRICPALKGVGATCMIDIMGMNTNTIGNAVYLLASLASI-NSVLP 158
DB 162 QYHRCGCVSIVMKVCPFLRGIGYICCTCTAIFAIYFNALIAQVFAIYLSKIMSEVP 221
QY 159 WTSQDNEMWTPCTP---VTSPTQPNSTPAKEFFERVNLBOHKSNGLDGMPKPSLA 215
DB 222 MASCGNPMWTPRCSDDLNTISRNGTPPLTPPSEYLLVLEQKSTGDDLDGAVTSM 281
QY 216 LCVFGEVFLVYFSLMKGVRSAGKVVWYATALAPYVLLILLANGVTLPGATEGIRYVLP 275
DB 282 VCLLAVFIWYFALMKGPSSGKIYVWTATAYIILSILLIRGLLPGAKNGLYYVTPD 341
QY 276 WHKLOSKYVDAASQIFPSLPGFGTLLALSSYNKFNNNCRDALITSINCLTSFLAG 335
DB 342 FEKLDPAAVMSAAQIFPSLPGFGVLLALSSYNFNNNCRDAVTTISINCAISFSG 401
QY 336 FVIFSVLGYMAHVONKSIE-VGLEBPGLVFIYVPEAATMGVSWAIIFFMLTLTGL 394
DB 402 CVFESTLIGMSLTLTKPIWVGEHDSALFIYVPAQALTMQYSCWMSIFEFVMLTTGL 461
QY 395 DSTFGGLEAVTTALCDEYPRVLGRHREYVAVALLFTYICALPTTYGGVYLVDLNLYG 454

DB 462 DSTFAGIEAFITGFCDE-SRFLSKNRKMFVLVICIITYLSEPAISYGGOVIFLDEYX 520
QY 455 PGLALFYFAFAEAGACWYGVDRSEYDRTMLGTHPGFWFRGWSYISPVFLVLFVS 514
DB 521 VLSVLFVITCEHIAVCMFYGVDOFSKDIRAMIGFPGIYWRGWT-CSPVFISYFEMT 579
QY 515 VL-AHEEMLGEYTPSPMSITVGMWMTGTVSCIPLYIYKLLTPGNCINR1KTP 572
DB 580 VYNSRKPLOMSYTPPMWSVILGWFLRLSLVALIPFAIYLLSTGTLYERFRATIP 639
QY 573 E-----VTSIPPADST 583
DB 640 QQRNRSATSL-AADPT 654

RESULT 5
US-09-843-598-7
Sequence 7, Application US/09843598
Patent No. US20020010944A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESERT GENES, PROTEINS, AND MODULATORY
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 01997/525002
CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 671
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-843-598-7

Query Match 50.0%; Score 1571.5; DB 10; Length 671;
Best Local Similarity 48.5%; Pred. No. 1.1e-132;
Matches 299; Conservative 110; Mismatches 162; Indels 45; Gaps 11;

QY 9 APTAPPDLPATTAAKRSRSVVS-----LTPARQ-----RE 39
DB 43 APTA-SEVWPLSVADKPLTLVSTSHSIDPNEPIALGSLTPKBEYVALRRSSMVAD 101
QY 40 TWAKKAEPFLAVVGAFAVDLGNWREPYICYONGGAFLLPYCYMLLFGGLPFFLELALG 99
DB 102 KWATKMEFLAVVGAFAVDLGNWREPYICYONGGAFLLPYCYMLLFGGLPFFLELALG 161
QY 100 QYHRCGLTLMKRICPALKGVGATCMIDIMGMNTNTIGNAVYLLASLASI-NSVLP 158
DB 162 QYHRCGCVSIVMKVCPFLRGIGYICCTCTAIFAIYFNALIAQVFAIYLSKIMSEVP 221
QY 159 WTSQDNEMWTPCTP---VTSPTQPNSTPAKEFFERVNLBOHKSNGLDGMPKPSLA 215
DB 222 MASCGNPMWTPRCSDDLNTISRNGTPPLTPPSEYLLVLEQKSTGDDLDGAVTSM 281
QY 216 LCVFGEVFLVYFSLMKGVRSAGKVVWYATALAPYVLLILLANGVTLPGATEGIRYVLP 275
DB 282 VCLLAVFIWYFALMKGPSSGKIYVWTATAYIILSILLIRGLLPGAKNGLYYVTPD 341
QY 276 WHKLOSKYVDAASQIFPSLPGFGTLLALSSYNKFNNNCRDALITSINCLTSFLAG 335
DB 342 FEKLDPAAVMSAAQIFPSLPGFGVLLALSSYNFNNNCRDAVTTISINCAISFSG 401
QY 336 FVIFSVLGYMAHVONKSIE-VGLEBPGLVFIYVPEAATMGVSWAIIFFMLTLTGL 394
DB 402 CVFESTLIGMSLTLTKPIWVGEHDSALFIYVPAQALTMQYSCWMSIFEFVMLTTGL 461
QY 395 DSTFGGLEAVTTALCDEYPRVLGRHREYVAVALLFTYICALPTTYGGVYLVDLNLYG 454
DB 462 DSTFAGIEAFITGFCDE-SRFLSKNRKMFVLVICIITYLSEPAISYGGOVIFLDEYX 520

[illegible]

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RESULT 6
US-09-795-693-24
: Sequence 24, Application US/09795693
: Patent No. US20020068710A1
: GENERAL INFORMATION:
: APPLICANT: Glucksmann, Maria A.
: TITLE OF INVENTION: 20665, 579, 17114, 23821, 33954, and
: TITLE OF INVENTION: 32613, No. US20020068710A1el Human Transporters
: FILE REFERENCE: 35800/209292
: CURRENT APPLICATION NUMBER: US/09/795,693-
: CURRENT FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 60/185,906
: PRIOR FILING DATE: 2000-02-29
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 624
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Pfam consensus sequence
: US-09-795-693-24

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Query Match	48.8%;	Score 1532.5;	DB 10;	Length 624;
Best Local Similarity	46.6%;	Pred. No. 3.2e-129;		
Matches 292;	Conservative 11;	Mismatches 129;	Indels 95;	Gaps 12

QY	38	REHMAKAEFFLLAVVGFADVLDLWNRPRPVCYKONGSGFLLPYCYMILLEGFLPFLEELA	97
Db	1	REHMSKLDLDFVLSVGFANGLGNWNRPRYCYKNGSGAFLLPYLLPLIVACIPPLFLELA	60
QY	98	LGQYHRCGLTLMKR-----ICPALKGVCYALCMIDIMGYNTPTIGMAVYVLIA	149
Db	61	LGQYHEGSIITVWRKKLDKDGKICPLPKRGKIGVSIVAFIIGIYVNIAMALXYL---	117
QY	150	LASINSLVMTSCDDNMNTPLCTPVTSPQTNPNSS-----TPAKEFE	192
Db	118	FSSFTTELPRMATICNNSMNTPNCEVERREKADNINGSLSAKSLNTDYTELETSVEEFWE	177
QY	193	RNVLEQHSNGSLDDMGPIKPLSLALCVFGEVFLVYFSLMKGYRS-AGRWVMTALAPVYL	251
Db	178	RGVLAKSESSGIEDLGELEKWEMLTCLLLAMIVYFCLMKGYKSSGSKVYVETAFPRVYL	237
QY	252	LILLAGVLLPGATFSIRYLLPRPKHKNQSNKSWDASQFEFSLGEGFGLTALSUNK	311
Db	238	YLLINGVLLPGADSDIKETLTPDSKLLDPQWMDAFTOLFSLGIGFGLTALASUNK	297
QY	312	FNNNCYRDALITSSINCLTSLFLAGVIFSVLGYNAH-VONKSIDE-----	355
Db	298	FHNKCYRDALIVSFINSTSLFLAGVIFSIILGPMANIVQEGGVDPENKILLLSRDLI	357
QY	356	-----VGL-----EGGLVFIYPRALMTG	377
Db	358	PHVNLISALTADYSYVDVISEVAESEFVGLGLCELEDDKVOAGGLAFIAYPRAYMLPL	417
QY	378	SVEMAIIFELMITLITGLDSTFGRLEAVYNTALACDEYPRVLR-HREVAVALITYFYCAL	436
Db	418	SPRWAVLFLMLMLITGLDSQFCGVCIGITLALYDEPILLKRVRELITLIVCVISFLGL	477
QY	437	PTTTCGGVYLVLDLNVY-GRGAILLEVFAEAGVCWYGVDSRESDVRTMLGHTPGWFV	495

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RESULT 7
US-10-156-239-24
: Sequence 24, Application US/10156239
: Publication NO. US20030036074A1
: GENERAL INFORMATION:
: APPLICANT: Glucksmann, Maria A.
: TITLE OF INVENTION: No. US20030036074A1 Nucleic Acid Sequences Encoding Human Tr
: TITLE OF INVENTION: Arpase Molecule, A Human Ubiquitin Hydrolase-Like Molecule,
: TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
: FILE REFERENCE: 35800/24/645
: CURRENT APPLICATION NUMBER: US/10/156,239
: CURRENT FILING DATE: 2002-05-24
: PRIOR APPLICATION NUMBER: 09/795,693
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 60/185,906
: PRIOR FILING DATE: 2000-02-29
: PRIOR APPLICATION NUMBER: 09/809,557
: PRIOR FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: 60/192,018
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: 09/808,568
: PRIOR FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 60/191,790
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: 09/808,767
: PRIOR FILING DATE: 2001-03-15
: PRIOR APPLICATION NUMBER: 60/191,781
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 624
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Pfam consensus sequence
: US-10-156-239-24

```

Query Match	48.88;	Score 1532.5;	DB 15;	Length 624;
Best Local Similarity	46.60;	Pred. No. 3.2e-129;		
Matches 292;	Conservative 111;	Mismatches 129;	Indels 95;	Gaps 12

```

Oy      38  RETMAKAEELLAVVEFADVLGNWVRPEYICVONGGAEFLPYCMLLEGLPEFLELA  97
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  RETMSKLDPELVLSVGEFAGLGNWVRPEYICVKNNGAEFLPYLLEFLVAGSIPLEFLELA  60

Oy      98  LGOYHRCGCLTLMKR-----ICPALKGVYACIMDITMGMYNTTIGMAYYILAS  149
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  LGOYTTEGSTYWRKKILDKGKICPLERGGIYASIVAFYIGLYVNIIMALAYYL--  117

Oy      150  LASINSVLPMTSCDNEMNTPLCTPYVTSPOINPNS-----TPAKEEFE  192
        : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      118  FSSFTTELPMACNWNMNPNCVEBEREAENSTNGSLASCKNLTDYLTERTSVEEWE  177

Oy      193  RNLLEQHSKNGDDMKPIKPSLALCPGVLYVYFSLMKGYRS-AGKVWVWTLAPVVL  251
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      178  RGVLKLSSESGIIDLCELMWELTLLALLAMIVYFCLMKGVKSSSGKVFYTAFFPVVL  237

Oy      252  LILLAGVTLPGATGESIRYLYLPEWHKLQNSKWIDAASQIFSLGPGFGLTALSSYNK  311
        : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 238 IYLLIRGVTLPGAADGKIFYPDPFSKLLDPQWIDAATQIFFSLGIGCVLIALASYNK 297
OY 312 FNNNCYRDALITSSINCLTSPFLAGFYIFSVLGYMAH-VONKSTIE----- 355
Db 298 FHNNCYRDALITSSINCLTSPFLAGFYIFSVLGYMAH-VONKSTIE----- 355
OY 356 -----VGL-----EGPGVIFYPEALATMNG 377
Db 358 PHYNLSALRADYSVYDVISEVAESEFVLGLACLEDELKQVQAGPGLAFIAYPEAVTMPL 417
OY 378 SVFMATIFFLMLITLGLDSTFGLEAVTALCDEYRVLGR-HREYFVAVLLFIYICAL 436
Db 418 SPFMATIFFLMLITLGLDSTFGLEAVTALCDEYRVLGR-HREYFVAVLLFIYICAL 436
OY 437 PTTTGGVYVLDLNNY-GRGLAIFVFAEAGVCWYGVDRFSDVFTMLGHPGWM 495
Db 478 FWTGEGIVFVFLFDYIYASGSFSLFVFEFCIAVAVYGDIDFYDITEMLGFRGLY 537
OY 496 RCMWSYISPVFLVFLVFSV-----LAHEML--GGEYTPSMSITVGMWMTGTVC 546
Db 538 KLCMKFVSPULLFLFIFSVIYGLKPLTYNNMIRKAEYVYPPMANALGMLLALSSMLC 597
OY 547 IPLYIYIKLLITPG-NCINRIKTIQRP 572
Db 598 VPLYIYIKLLSTEGDSLRLERLOKATTP 624

RESULT 8

US-10-199-485-24
Sequence 24, Application US/10199485
Publication No. US2003007626A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
FILE REFERENCE: 35800/249468
CURRENT APPLICATION NUMBER: US/10/199,485
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 09/795,693
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 624
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Pfam consensus sequence
US-10-199-485-24

Query Match 48.8%; Score 1532.5; DB 15; Length 624;
Best Local Similarity 46.6%; Pred. No. 3.2e-129;
Matches 292; Conservative 111; Mismatches 129; Indels 95; Gaps 12;

OY 38 RETWAKKAEFLAVGFAVDLGNWVRPPIYCYONGGAFILIPYCVMLTFLGFLPFL 97
Db 1 RETWAKKAEFLAVGFAVDLGNWVRPPIYCYONGGAFILIPYCVMLTFLGFLPFL 97
OY 98 IGOYHRCGCLTLTKR-----ICPALKGVGAICMIDYMGMYNTIIGNAVYLIAS 149
Db 61 IGOYHRCGCLTLTKR-----ICPALKGVGAICMIDYMGMYNTIIGNAVYLIAS 149
OY 150 LASINSVLPWTSCDNEMNPLCTPVYSPQTNPNSS-----TPAKEFE 192
Db 118 FSSFTTELPAWTCNNMNTPCNVEEREAENSTNGSIALSKNLTDTYLETSPVEE 177
OY 193 RNVLEQHSKNGLDMPGPIKPSIALCVGCVFLVYFSLMKVRS-AGVYVWVTLAPYVL 251
Db 178 RGVLLKSSGSEDIEDLRLWELTCLLALWIVVYFCLMKGVKSGSKVVFETATFPYVL 237

OY 252 LILLARGVTLPGAATEGIRYRYLPEMHKLONSKVWIDAASQIFFSLGPGFTLLASYNK 311
Db 238 IYLLIRGVTLPGAADGKIFYPDPFSKLLDPQWIDAATQIFFSLGIGCVLIALASYNK 297
OY 312 FNNNCYRDALITSSINCLTSPFLAGFYIFSVLGYMAH-VONKSTIE----- 355
Db 298 FHNNCYRDALITSSINCLTSPFLAGFYIFSVLGYMAH-VONKSTIE----- 355
OY 356 -----VGL-----EGPGVIFYPEALATMNG 377
Db 358 PHYNLSALRADYSVYDVISEVAESEFVLGLACLEDELKQVQAGPGLAFIAYPEAVTMPL 417
OY 378 SVFMATIFFLMLITLGLDSTFGLEAVTALCDEYRVLGR-HREYFVAVLLFIYICAL 436
Db 418 SPFMATIFFLMLITLGLDSTFGLEAVTALCDEYRVLGR-HREYFVAVLLFIYICAL 436
OY 437 PTTTGGVYVLDLNNY-GRGLAIFVFAEAGVCWYGVDRFSDVFTMLGHPGWM 495
Db 478 FWTGEGIVFVFLFDYIYASGSFSLFVFEFCIAVAVYGDIDFYDITEMLGFRGLY 537
OY 496 RCMWSYISPVFLVFLVFSV-----LAHEML--GGEYTPSMSITVGMWMTGTVC 546
Db 538 KLCMKFVSPULLFLFIFSVIYGLKPLTYNNMIRKAEYVYPPMANALGMLLALSSMLC 597
OY 547 IPLYIYIKLLITPG-NCINRIKTIQRP 572
Db 598 VPLYIYIKLLSTEGDSLRLERLOKATTP 624

RESULT 9

US-09-795-232-2
Sequence 2, Application US/09795232
Patent No. US20010012627A1
GENERAL INFORMATION:
APPLICANT: Anthony M. Brown
APPLICANT: Conrad Gerald Chapman
APPLICANT: Israel Simon Gloger
APPLICANT: Joanne Rachel Evans
APPLICANT: William Cairns
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30176-D1
CURRENT APPLICATION NUMBER: US/09/795,232
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/182,728
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 9818890.7
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 797
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-795-232-2

Query Match 43.6%; Score 1369.5; DB 10; Length 797;
Best Local Similarity 45.0%; Pred. No. 2e-114;
Matches 238; Conservative 105; Mismatches 169; Indels 41; Gaps 4;

OY 36 RORETWAKKAEFLAVGFAVDLGNWVRPPIYCYONGGAFILIPYCVMLTFLGFLPFL 95
Db 189 KARGNMSSKRDILTSVNGVAVGNNWVRPPIYLAFOGNGGAFILIPYLAAGLPFLFLE 248
OY 96 LAIGYHRCGCLTLTKR-----ICPALKGVGAICMIDYMGMYNTIIGNAVYLIAS 155
Db 249 VSLGOFASOGPVSWKAI-PALOGGCIAMLLISVLAIAVYNYICTLFLYFASFV---S 304
OY 156 VLPWTSCDNEMNPLCTPVY-----SPQTN 180
Db 305 VLPWGSNNPWNTPPECKDKTKLLDSCVTSIDHKKIOIKNSTFCMTIAYPNVTWNTSOAN 364
OY 181 PNSTPAKEFFEERNVLEOHKSNGLDMPGPIKPSIALCVGCVFLVYFSLMKGVRSAGKV 240

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Db      365 KTFVAGSESEYFYFLK--ISAGIEYGEIRWPLALCLFLAWVIYASLAKGKTSKVV 422
Qy      241 WYATAPYVVLILLILARGLTLPAGTEGIRKYITLPEMHKIONSKWIDAQJFFSLGPGF 300
Db      423 YFTATFFPYVVLILLIRGVTLPAGAGIWFYITTPKWEKLTNATWKDQTOFFSLASAM 482
Qy      301 GTLLALSSYNNKNNCYRDALITSSINCLTSFLAGVIFSVGLYMAHVNKISIEEVLGEG 360
Db      483 GGLITLSSYNNKNNCYRDALITSSINCLTSFLAGVIFSVGLYMAHVNKISIEEVLGEG 542
Qy      361 PELVITVPEALITATMGVFAIIFFLMILITGLDSTEGEAVTALCDEXPRVLGRHR 420
Db      543 POLAVVYPEALTRPLSPFMAIIFFLMILITGLDSTEGEAVTALCDEXPRVLGRHR 602
Qy      421 EEFVAVLLFIYICALPTTGGVYLVLDLNVYGGILTFVFPAAAGVGVGVDRPS 480
Db      603 PVFTAGCCICFTMGFPMTGOGITMFOVLVDYTAASVALYITAIREFLVGISTVYGLQRC 662
Qy      481 EDVRTMLGHTPGMFWRTGMSYISPVLLVLFVSVLAHEMLGCEYTPSMISITVGWWT 540
Db      663 EDIEMWIGFQPNIFMKVCAVFAVTPILTFILCFSEFYQWEPMTYGSYRPNMNSVLGML 722
Qy      541 GTTVCSCIPLYITKLLITPGNCINRIKITQPE 573
Db      723 ACSYIMIPIMFYIKMHLAPGRFIERLKLACSPQ 755

RESULT 10
US-09-815-923-14
: Sequence 14, Application US/09815923
: Publication No. US20020197644A1
: GENERAL INFORMATION:
: APPLICANT: GILL, Sargeet S.
: APPLICANT: Ross, Linda S.
: TITLE OF INVENTION: The Regents of the University of California
: TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1e1
: FILE REFERENCE: 023070-093800US
: CURRENT APPLICATION NUMBER: US/09/815,923
: CURRENT FILING DATE: 2001-03-23
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 14
: LENGTH: 597
: TYPE: PRT
: ORGANISM: Manduca sexta
: FEATURE:
: OTHER INFORMATION: GABA transporter
: 09-815-923-14

Query Match      41.5%; Score 1302; DB 11; Length 597;
Best Local Similarity 42.5%; Pred. No. 1.6e-108;
Matches 248; Conservative 108; Mismatches 183; Indels 44; Gaps 8;

Qy      18 PATTAQKRSYVSLTPARQRETMAKKAFFLLAVGVAVDLGNVWRPFYICQNGGAGFL 77
Db      23 PSDVAVAKSN-----LPERGSMASKLDLITLSVIGLIGGNVWRPFYILCKNGGAGFL 74
Qy      78 IPYCVMLLFGGLPLFLELALGOYHRCCGLLMKRICALGVGYATIMIDIYMGMYNT 137
Db      75 IPYELTLELAGIPMEFLMAGOMLTIGLGVFK-IAPIFGIGGYAAVMSGMNVYIV 133
Qy      138 IIGNAVYLLASLINSVLPMTSCDNEMNTPLCPVTSQPTNP----- 182
Db      134 ILANAIIFEFMS--NSDVPWRNCDNTWNTATC--VNPYDRKMLTJCSWSSLDGDNSTFCT 187
Qy      183 -----SSTPAKEFEFRNVLEQHSNGLDDMGPIKPSLALCVGFVLYVSLMKG 232
Db      188 LNGRNVSAVSLDPYKKEWERALQ--ISSGIEHGNIRNRELAGLILLVWVLCYCIK 245
Qy      233 VRSAGKYVWATALAPYVVLILLARGLTLPAGTEGIRKYITLPEMHKIONSKWIDAQJ 292

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Db      246 VMTGKVYVYFALPFYLLTVLLIRGITLPAGMEGIRKFWMDNMMSKILESEVVIDAVTQI 305
Qy      293 FESLGRPGFTLLALSYNNKNNCYRDALITSSINCLTSFLAGVIFSVGLYMAHVNK 352
Db      306 FESYIGLGTLLVALGSYNNKNNCYRDALITSSINCLTSFLAGVIFSVGLYMAHVNK 365
Qy      353 IEEVLEGGGLVFIYPEALITATMGVFAIIFFLMILITGLDSTEGEAVTALCDEX 412
Db      366 VAEVASAGGLAFNAVPSAVDLPAGAPLMSCLFFMILLITGLDSTEGEAVTALCDEX 425
Qy      413 PVILGRHREVEVAVLLFIYICALPTTGGVYLVLDLNVY--POLAILFVFAEAGVC 471
Db      426 PKLLRRRKEIFAIICIIISYLVGLSCISEGMYVFOIIDSYAVSGFCLLIFFECSVIS 485
Qy      472 WYGVDRSEEDVRTMLGHTPGMFWRTGMSYISPVLLVLFVSVLAHEMLGCEYTPSM 531
Db      486 WAFGVNRFYDGIKEMIGITPTIMMFCWGGFTPAICISVFIFNLQWMPRTKYMYEYPM 545
Qy      532 SITVGMVMTGTTVSCIPLYITKLLITPGNCINRI-KTQORPE 573
Db      546 SHAFGMFTALSSMLCIPGYMIYLMVTRGTQWEKFKHIVRIPE 588

RESULT 11
US-09-919-039-378
: Sequence 378, Application US/09919039
: Publication No. US20030108871A1
: GENERAL INFORMATION:
: APPLICANT: Kaser, Matthew R.
: TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
: FILE REFERENCE: PA-0035 US
: CURRENT APPLICATION NUMBER: US/09/919,039
: CURRENT FILING DATE: 2002-09-09
: PRIOR APPLICATION NUMBER: 60/222,113
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 401
: SOFTWARE: PERL Program
: SEQ ID NO 378
: LENGTH: 614
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20030108871A1 5834958CD1
: US-09-919-039-378

Query Match      39.7%; Score 1247.5; DB 12; Length 614;
Best Local Similarity 41.1%; Pred. No. 1.3e-103;
Matches 242; Conservative 116; Mismatches 208; Indels 23; Gaps 9;

Qy      7 PPAPTAAPPDLPATTAQKRSYVSLTPARQRETMAKKAFFLLAVGVAVDLGNVWRPFY 66
Db      12 PPAVSWVEBEGEKLDQEDQEDOV-----KDRGQNTKMEFVLSVAGELTIGLGNVWRPFY 64
Qy      67 ICYONGGAGFLIPYCVMLLFGGLPLFLELALGOYHRCCGLLMKRICAPLAKGVGYATIM 126
Db      65 LCYKNGGAGFAFPYRIFPFVGVGIPVFELEVALGOYTSQGSYTAAMKICPLRGIGLASVY 124
Qy      127 IDIYGMVYNNIIGNAVYLLASLINSVLPMTSCDNEMNTPLCTPVTSQ-----TNP- 181
Db      125 IESYLVNYYIIILAMALFYL--FSSFTSELPTWCNNFMNTEHCTDELNHSAGATVPF 181
Qy      182 -NSSPAKEFEFRNVLEQHSNGLDDMGPIKPSLALCVGFVLYVSLMKGVSAAGVY 240
Db      182 ENFTSPVNEFERRVL--GITSIHDLGSLWELALCLLLAMVICYFCITMGVASTGVY 239
Qy      241 WYATAPYVVLILLILARGLTLPAGTEGIRKYITLPEMHKIONSKWIDAQJFFSLGPGF 300
Db      240 YFTATFFPYVVLILLIRGVTLPAGAGIWFYITTPKWEKLTNATWKDQTOFFSLASAM 299
Qy      301 GTLLALSSYNNKNNCYRDALITSSINCLTSFLAGVIFSVGLYMAHVNKISIEEVLGEG 360
Db      300 GCLTALAGSYNNKNNCYRDALITSSINCLTSFLAGVIFSVGLYMAHVNKISIEEVLGEG 359

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RESULT 14
 US-09-815-923-6
 : Sequence 6, Application US/09815923
 : Publication No. US20020197644A1
 : GENERAL INFORMATION:
 : APPLICANT: Gill, Sarjeet S.
 : APPLICANT: Ross, Linda S.
 : APPLICANT: The Regents of the University of California
 : TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1
 : TITLE OF INVENTION: Target Sites for Insecticides
 : FILE REFERENCE: 023070-093800US
 : CURRENT APPLICATION NUMBER: US/09/815,923
 : CURRENT FILING DATE: 2001-03-23
 : NUMBER OF SEQ ID NOS: 20
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 6
 : LENGTH: 556
 : TYPE: PRT
 : ORGANISM: Manduca sexta
 : FEATURE:
 : OTHER INFORMATION: proline transporter
 -09-815-923-6

```

: APPLICANT: GONG, Fangcheng et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CC001191
: CURRENT APPLICATION NUMBER: US/09/818,656A
: CURRENT FILING DATE: 2000-03-28
: NUMBER OF SEQ ID NOS: 103
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 437
: TYPE: PRT
: ORGANISM: Homo sapien
: US-09-818-656A-4

```